

FORM PTO-1449 (Modified)

ATTY. DOCKET NO.
24737-1906C

SERIAL NO.
09/709,905

LIST OF PATENTS AND PUBLICATIONS FOR
APPLICANT'S INFORMATION DISCLOSURE
STATEMENT

APPLICANT
Ramnarayan et al.

FILING DATE
November 10, 2000

GROUP
1631



U.S. PATENT DOCUMENTS

EXAMINER INITIAL	DOCUMENT NUMBER	DATE	NAME	CLASS	SUB CLASS	FILING DATE
NONE						

FOREIGN PATENT DOCUMENTS

DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB CLASS	Translation Yes No
NONE					

OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

JSB	A	Koehl <i>et al.</i> , "A brighter future for protein structure prediction", <i>Nature Structure Biology</i> , 6(2):108-111, 1999
JSB	B	Sternberg <i>et al.</i> , "Progress in protein structure prediction: assessment of CASP3", <i>Current Opinion in Structural Biology</i> , 9:368-373, 1999

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JSB. Brum

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11/27/02

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Sheet 1 of 1

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U.S. PATENT DOCUMENTS

EXAMINER INITIAL	DOCUMENT NUMBER	DATE	NAME	CLASS	SUB CLASS	FILING DATE

FOREIGN PATENT DOCUMENTS

	DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB CLASS	Translation Yes No
JLB	AA 9 5 1 4 7 9 1	06/01/95	PCT			

OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

	None

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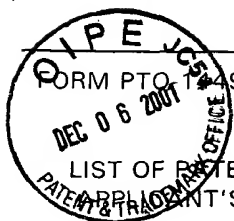
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Title: **USE OF COMPUTATIONALLY DERIVED PROTEIN STRUCTURES OF GENETIC POLYMORPHISMS IN PHARMACOGENOMICS FOR DRUG DESIGN AND CLINICAL APPLICATIONS**



FORM PTO 1549 (Modified) LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT	ATTY. DOCKET NO. 24737-1906C	SERIAL NO. 09/709,905
	APPLICANT Ramnarayan <i>et al.</i>	
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U.S. PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER							DATE	NAME	CLASS	SUB CLASS	FILING DATE
JLB	A	5	3	3	1	5	7	3	07/19/94	Balaji <i>et al.</i>			

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JLB	B	9	5	0	6	2	9	3	03/02/95	PCT				
JLB	C	9	5	1	4	0	2	8	05/26/95	PCT				
JLB	D	9	8	0	6	0	4	8	02/12/98	PCT				
JLB	E	9	8	1	3	7	8	1	04/02/98	PCT				
JLB	F	9	8	5	4	6	6	5	12/03/98	PCT				

OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

JLB	G	Abdel-Meguid, S.S. <i>et al.</i> "An orally bioavailable HIV-1 protease inhibitor containing an imidazole-derived peptide bond replacement: crystallographic and pharmacokinetic analysis," <i>Biochemistry</i> 33(39):11671-11677 (1994)
	H	Blaney, R. "Molecular modelling in the pharmaceutical industry," <i>Chemistry and Industry. Chemistry and Industry Review</i> 23(4):791-4 (1990). <i>not considered no copy provided</i>
	I	Bohm, G. "New approaches in molecular structure prediction," <i>Biophysical Chemistry</i> 59:1-32 (1996) <i>not considered no copy provided</i>
JLB	J	Thompson, S.K. <i>et al.</i> "Rational design, synthesis, and crystallographic analysis of a hydroxyethylene-based HIV-1 protease inhibitor containing a heterocyclic P1'-P2' amide bond isoster," <i>Journal of Medicinal Chemistry</i> 37(19):3100-3107 (1994).

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JLB. Bruce

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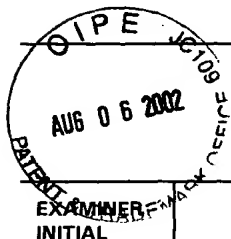
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* JB	AA	5	3	1	7	0	9	7	05/31/94	Miller <i>et al.</i>	536	24.31	10/07/91
* JB	AB	5	4	9	5	4	2	3	02/27/96	DeLisi <i>et al.</i>	364	496	10/25/93
* JB	AC	5	5	9	3	9	5	9	01/14/97	Miller <i>et al.</i>	514	8	10/14/93
* JB	AD	5	6	2	4	8	1	7	04/29/97	Miller <i>et al.</i>	435	69.1	04/28/94
* JB	AE	5	6	9	9	2	6	8	12/16/97	Schmidt	364	496	06/07/95
* JB	AF	5	9	6	8	7	3	7	10/19/99	Ali-Osman <i>et al.</i>	435	6	11/12/96
* JB	AG	5	9	7	8	7	4	0	11/02/99	Armistead <i>et al.</i>	702	19	08/09/95
* JB	AH	6	1	2	8	5	8	2	10/03/00	Wilson <i>et al.</i>	702	27	04/30/96

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None														

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* JB	AI	Baker <i>et al.</i> , "Protein Structure Prediction and Structural Genomics", Science, 294:93-96 (2001)											
* JB	AJ	Hess <i>et al.</i> , "Impact of Pharmacogenomics on the Clinical Laboratory", Mol. Diagn., 4(4):289-98 (1999)											
* JB	AK	Hess <i>et al.</i> , "Gene Therapy Monitoring: Clinical Monitoring for Efficacy and Potential Toxicity", Mol. Diagn., 2(2):147-155 (1997)											

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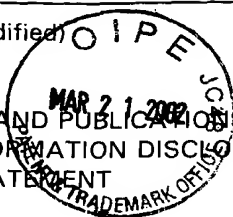
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* References are not included.

U.S. PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER							DATE	NAME	CLASS	SUB CLASS	FILING DATE
*	AA	5	7	1	2	1	4	5	01/27/98	Houghton <i>et al.</i>	435	219	09/06/96

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		DOCUMENT NUMBER							DATE	COUNTRY	CLASS	SUB CLASS	Translation Yes No	

OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

*	AB	Ajay <i>et al.</i> , Computational Methods to Predict Binding Free Energy in Ligand-Receptor Complexes, <u>Journal of Medicinal Chemistry</u> , 38(26):4953-4967 (1995).
*	AC	Balaji <i>et al.</i> , Conformational studies on model peptides with 1-aminocyclopropane 1-carboxylic acid residues, <u>Pept. Res.</u> 7(2):60-71 (1994).
*	AD	Balaji <i>et al.</i> , Conformational studies on model peptides with 1-aminocyclobutane 1-carboxylic acid residues, <u>Pept. Res.</u> 8(3):178-86 (1995).
*	AE	Balasubramaniam <i>et al.</i> , [D-TRP ³²]Neuropeptide Y: A Competitive Antagonist of NPY in Rat Hypothalamus, <u>J. Med. Chem.</u> 37(6):811-815 (1994).
*	AF	Böhm, Prediction of binding constants of protein ligands: A fast method for the prioritization of hits obtained from de novo design or 3D database search programs, <u>Journal of Computer-Aided Molecular Design</u> , 12:309-323 (1998).
*	AG	Checa <i>et al.</i> , Assessment of Solvation Effects on Calculated Binding Affinity Differences: Trypsin Inhibition by Flavonoids as a Model System for Congeneric Series, <u>J. Med. Chem.</u> 40:4136-4145 (1997).
*	AH	Daniels, Blood group polymorphisms: molecular approach and biological significance, <u>Transfus. Clin. Biol.</u> 4:383-390 (1997).

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* JB	AI	Das <i>et al.</i> , Crystal Structures of 8-Cl and 9-Cl Complexed with Wild-type HIV-1 RT and 8-Cl TIBO Complexed with the Tyr181Cys HIV-1 RT Drug-resistant Mutant, <u>J. Mol. Biol.</u> 264:1085-1100 (1996).
* JB	AJ	Eldridge <i>et al.</i> , Empirical scoring functions: I. The development of a fast empirical scoring function to estimate the binding affinity of ligands in receptor complexes, <u>Journal of Computer-Aided Molecular Design.</u> 11:425-445 (1997).
* JB	AK	Fox, S. Pharmacogenomics Thrives in Europe. <u>Genetic Engineering News</u> , June 15, 1999.
* JB	AL	Leheny <i>et al.</i> Symposium on Resistance Highlights New Trends in AIDS Treatments: Implications for BioChem Pharma and Others, <u>Hambrecht & Quist LLC Institutional Research</u> , pp. 1-7 (1997). <i>not considered</i> <i>no copy provided</i>
* JB	AM	Manavalan <i>et al.</i> , Location of Potential Binding Sites on Deoxy Hemoglobin for the Design of Antigelling Agents, <u>J. Mol. Biol.</u> 223:791-800 (1992).
* JB	AN	Munson <i>et al.</i> , Identification of an extracytoplasmic region of H ⁺ , K ⁽⁺⁾ -ATPase labeled by a K ⁽⁺⁾ -competitive photoaffinity inhibitor, <u>J. Biol. Chem.</u> 266(28):18976-88 (1991).
* JB	AO	Novotny <i>et al.</i> , Empirical Free Energy Calculations: A Blind Test and Further Improvements to the Method, <u>J. Mol. Biol.</u> 268:401-411 (1997).
* JB	AP	Press Release, Structural Bioinformatics Inc. and Cyberchemics, Inc. Collaborate to Speed the Generation of Hepatitis C Viral Protease Inhibitors, <u>SBI News</u> . Located at http://strubix.com/press/press5.html , pp. 1-2 (1997).
* JB	AQ	Press Release, Structural Bioinformatics Inc. Selects IBM RS/6000 SP to Speed Drug Design, <u>SBI News</u> . Located at http://strubix.com/press/press11.html , pp. 1-2 (1997).
* JB	AR	Press Release, SBI Protein Models & Ligand Binding for Novel Viral Enzyme Validated, <u>SBI News</u> . Located at http://strubix.com/press/press32.html , pp. 1-2 (1999).
* JB	AS	Press Release, Structural Bioinformatics Inc. Generates Antiviral Lead Compound from Gene Sequence to Achieve Milestone in Biochem Pharma Collaboration, <u>SBI News</u> . Located at http://strubix.com/press/press20.html , pp. 1-2 (1998).
* JB	AT	Press Release, SBI's Protein Structure Directed Combinatorial Chemistry Cuts Time and Cost 100X for Synthesis of New Anti-Inflammatory Drug Lead Molecules (TNF Receptor Antagonists), <u>SBI News</u> . Located at http://strubix.com/press/press19.html , pp. 1-2 (1998).

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*	AU	Press Release, Structural Bioinformatics Inc. Generates Non-Peptide Lead Molecules Active Against the EPO Receptor from Gene Sequence Data, <u>SBI News</u> , Located at http://strubix.com/press/press22.html , pp. 1-2 (1998).
*	AV	Press Release, Structural Bioinformatics Inc. Develops Small-Molecule Antagonists of BCL-2 Gene Product, an Important Apoptosis-Related Protein Target in the Pathology of Human Cancers, <u>SBI News</u> , Located at http://strubix.com/press/press26.html , pp. 1-2 (1999)
*	AW	Radack <i>et al.</i> , Intercorrelations and sources of variability in three mutagenicity assays: a population-based study, <u>Mutation Research</u> , 350 (1996); pp. 295-306.
*	AX	Radmer <i>et al.</i> , The application of three approximate free energy calculations methods to structure based ligand design: Trypsin and its complex with inhibitors, <u>Journal of Computer-Aided Molecular Design</u> , 12:215-227 (1998).
*	AY	Ramnarayan <i>et al.</i> , Antibody humanization predicted by computer graphic analysis, <u>Am. Biotechnol. Lab.</u> 13(9):26,28 (1995).
*	AZ	Ramnarayan <i>et al.</i> , Conformational studies on model dipeptides of Gly, L-Ala and their C α -substituted analogs, <u>Int. J. Pept. Protein Res.</u> 45(4):366-76 (1995).
*	BA	Ramnarayan <i>et al.</i> , Characterization of a Linear Pentapeptide Containing Two Consecutive β -Turns, <u>Pept. Res.</u> 7(5):270-8 (1994).
*	BB	Regalado, Inventing the pharmacogenomics business, <u>Am. J. Health-Syst. Pharm.</u> 56:40-50 (1999).
*	BC	Rao <i>et al.</i> , Conformational Studies on β -Amino Acid-Containing Peptides. I., <u>Pept. Res.</u> 5(6):343-50 (1992).
*	BD	Shafer <i>et al.</i> , Multiple Concurrent Reverse Transcriptase and Protease Mutations and Multidrug Resistance of HIV-1 Isolates from Heavily Treated Patients, <u>Annals of Internal Medicine</u> , 128(11):906-11 (1998).
*	BE	Skaletsky <i>et al.</i> , Accessing three-dimensional chemical information in antibody molecules, <u>Am. Biotechnol. Lab.</u> 11(5):10-3 (1993).
*	BF	Shenderovich, <i>et al.</i> , "Structural Pharmacogenic Approach to the Evaluation of Drug Resistant Mutations and HIV-1 Protease", <u>Journal of Clinical Ligand Assay</u> , 24(2):140-144 (2001)

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*	BG	Smith <i>et al.</i> , Molecular modeling of HIV-1 reverse transcriptase drug-resistant mutant strains: implications for the mechanism of polymerase action, <u>Protein Engineering</u> , 10(12):1379-83 (1997).
*	BH	Spear, Viewpoint - Pharmacogenomics: Today, Tomorrow, and Beyond, <u>Drug Benefit Trends</u> , 11(2):53-54 (1999).
*	BI	Takamatsu <i>et al.</i> , A New Method for Predicting Binding Free Energy Between Receptor and Ligand, <u>Proteins: Structure, Function, and Genetics</u> , 33:62-73 (1998).
*	BJ	Tantillo <i>et al.</i> Locations of Anti-AIDS Drug Binding Sites and Resistance Mutations in the Three-dimensional Structure of HIV-1 Reverse Transcriptase, <u>J. Mol. Biol.</u> , 243:369-387 (1994).
*	BK	Vajda <i>et al.</i> Empirical potentials and functions for protein folding and binding, <u>Theory and Simulation</u> , 7:222-228 (1997).
*	BL	Wang and Kollman, "Computational study of protein specificity: The molecular basis of HIV-1 protease drug resistance", <u>PNAS</u> , 98(26):14937-14942 (2001). <i>not considered</i> <i>no copy provided</i>
*	BM	Weng <i>et al.</i> , Prediction of protein complexes using empirical free energy functions, <u>Protein Science</u> , 5:614-626 (1996). <i>not considered</i> <i>no copy provided</i>
*	BN	Zhu <i>et al.</i> , Identification of two new hydrophobic residues on basic fibroblast growth factor important for fibroblast growth factor receptor binding, <u>Protein Engineering</u> , 11(10):937-40 (1998).
*	BO	Zhu <i>et al.</i> , Analysis of high-affinity binding determinants in the receptor binding epitope of basic fibroblast growth factor, <u>Protein Eng.</u> , 10(4):417-21 (1997).
*	BP	Zhu <i>et al.</i> , Glu-96 of basic fibroblast growth factor is essential for high affinity receptor binding. Identification by structure-based site-directed mutagenesis, <u>J. Biol. Chem.</u> , 270(37):21869-74 (1995).

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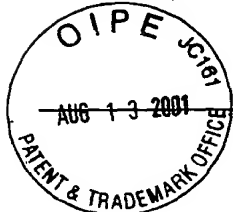
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* JB	4 2 0 8 4 7 9	06/17/80	Zuk <i>et al.</i>	435	7	07/14/77
* JB	4 2 2 0 4 5 0	09/02/80	Maggio	23	230	04/05/78
* JB	4 2 3 3 4 0 1	11/11/80	Yoshida <i>et al.</i>	435	7	07/14/77
* JB	4 2 3 3 4 0 2	11/11/80	Maggio <i>et al.</i>	435	7	04/05/78
* JB	4 2 7 7 4 3 7	07/01/81	Maggio	422	61	12/10/79
* JB	4 3 8 5 1 2 6	05/24/83	Chen <i>et al.</i>	436	518	03/19/79
* JB	4 3 9 7 9 5 6	08/09/83	Maggio	436	34	12/10/81
* JB	4 7 8 6 4 7 1	11/22/88	Jones <i>et al.</i>	422	61	10/21/83
* JB	4 7 8 9 6 3 1	12/06/88	Maggio	435	7	02/17/84
* JB	4 8 2 8 9 8 1	05/09/89	Maggio	435	7	08/24/83
* JB	4 8 5 9 6 1 0	08/22/89	Maggio	436	518	09/12/86
* JB	5 0 7 9 1 4 2	01/07/92	Coleman <i>et al.</i>	435	7.92	01/23/87
* JB	5 2 1 5 8 9 9	06/01/93	Dattagupta	435	6	08/23/90
* JB	5 3 3 1 5 7 3	07/19/94	Balaji <i>et al.</i>	364	500	12/14/90
* JB	5 5 7 1 8 2 1	11/05/96	Chan <i>et al.</i>	514	312	05/20/94
* JB	5 5 7 9 2 5 0	11/26/96	Balaji <i>et al.</i>	364	496	04/24/95
* JB	5 6 1 2 8 9 5	03/18/97	Balaji <i>et al.</i>	364	496	04/21/95
* JB	5 7 1 2 1 4 5	01/27/98	Houghton <i>et al.</i>	435	219	09/06/96
* JB	5 8 0 8 9 6 9	09/15/98	Arnaud <i>et al.</i>	367	103	12/04/95
* JB	5 8 3 7 4 6 4	11/17/98	Capon <i>et al.</i>	435	6	01/29/97
* JB	5 8 4 6 7 6 3	12/08/98	Lee <i>et al.</i>	435	69.1	05/13/94
* JB	5 9 1 0 4 7 8	06/08/99	Hlavka <i>et al.</i>	514	9	09/20/96

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*	JB		0	0	5	7	3	0	9	09/28/00	PCT			
*	JB		9	7	2	7	3	1	9	07/31/97	PCT			
*	JB		9	7	2	7	4	8	0	07/31/97	PCT			
*	JB		9	9	0	6	5	9	7	02/11/99	PCT			

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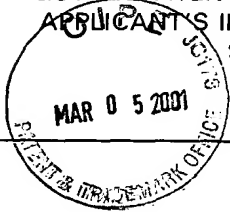
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











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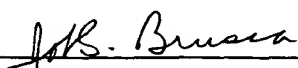
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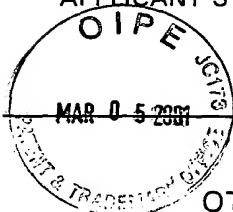
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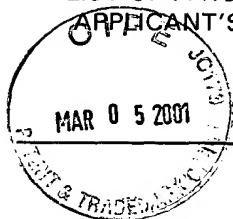
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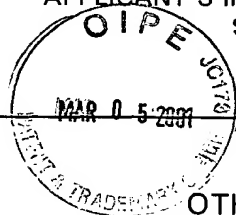
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LIST OF PATENTS AND PUBLICATIONS FOR
APPLICANT'S INFORMATION DISCLOSURE
STATEMENT



OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

* JB	Vajda <i>et al.</i> Empirical potentials and functions for protein folding and binding, <u>Theory and Simulation</u> , 7:222-228 (1997).
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